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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STSNNTKETSDLLREIAADSIVLLKNKNNYLTSKERRQYHVIGPNAKAKTSSGGGSASMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIEFPGPTRWRTRALVSHSLNSREQITTEDVDDRVRQVLKMIKFVVDNLEKTGIVENGPE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLEMPGPPRFRGETLKFNVSNGKPFIHV--IDQRAREVLQFVK----KCAASGVTENGPE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPFLAGLGAAALIRGIQSTGVQATIKHFLCNDQEDRRMMVQSIVTERALREIYALPFQIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQVYGSGLFYLNDELIIDQKHNQERGSFCFGAGTKERTKKLTLKKGQVYNVRVEYGSGPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P--VEERSEDEEPFHVTKVNRSNVHLFDFKHEKVDPKNPYFFVTLTGQYVPQEDGDYIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPGTPNRQHIDELF----FTKTDMHLVDYYHPKAADT---WYADMEGTYTADEDCTYELG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKHANPVCIMTAYNKVNGDHCSQSKKLLIDILRDEWKWDGMLMSDWFGTYTTAAAIKNGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRDSQPGAFMTAYNGINGVSCSENPKYLDGMLRKEWGWDGLIMSDWYGTYSTTEAVVAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPYLAGMATSSVVKGMQGEGIAATVKHFVCNDLEDQRFSSNSIVSERALREIYLEPFRLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACFPCGTSLGSTFNQTLLEEAGKMMGKEAIAKSAHVILGFTINMQRSPLGGRGFESIGE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTVNNTPETAALLRKVGNEGIVLLKNENNVLPLSKKKKTLIVGPNAKQATYHGGGSAALR 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt SGCFPNGTGLASTFDRDLLETAGKLMAKESIAKNAAVILGPTTNMQRGPLGGRGFESFSE}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt MSKFDVEQLLSELNQDEKISLLSAVDFWHTKKIERLGIPAVRVSDGPNGIRGTKFFDGVP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MADIDVEAILKKLTLAEKVDLLAGIDFWHTKALPKHGVPSLRFTDGPNGVRGTKFFNGVP
                                                                                                                                               STANDARD;
                                                                                                                                             PRT;
                                                                                                                                             818 AA.
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Best Local S
Matches 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PE00933; Glyco_hydro_3; 1.
Pfam; PF01915; Glyco_hydro_3_C; 1.
PRINTS; PR00133; GLHYDRLASE3.
PROSITE; PS00775; GLYCOSYL_HYDROL_F3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
          417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Glycosidase. ACT_SITE 222 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 174:1478-1486(1992).

-i- FUNCTION: INVOLVED IN MODIFYING A VIR-INDUCING PLANT SIGNAL MOLECULE. HYDROLYZES CONIFERIN BUT NOT CELLOBIOSE.

-i- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-glucose residues with release of beta-D-glucose.

-i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
                                                                               358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M59852; AAA22082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Castle L.A., Smith K.D., Morris R.O.;
"Cloning and sequencing of an Agrobacterium tumefaciens
beta-glucosidase gene involved in modifying a vir-inducing plant
signal molecule.";
                                                                                                                                                361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001764; GH_3N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A42292; A42292.
                                                                                                                                                                                                                                                                            303 TAALLRKVGNEGIVLLKNENNVLPLSKKK--KTLIVGPNAKQATYHGGGSAALRAYYAVT 360
                                                                                                                                                                                                                                                                                                                                                           242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92165721; PubMed=1537792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
IDELFF---TKTDMHLVDYYHPKAADTWYADMEGTYTADEDCTYELGLVVCGTAKAYVDD
                                                                    PLEGIRAALSNANSLRHAVGCNNNRLIDVFSGE--MTVEYFKG---RGFESRPVHVETVE
                                                                                                                                                                                                          DRALIRQLGAEGAVLLKND-GVLPLAKSSFDQIAVIGPNAASARVMGGGSARIAAHYTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEAILKKLTLAEKVDLLAGIDFWHTKALPKHGVPSLRFTDGPNGVR-GTKFFNGVPAACF 64
                                                                                                                                      PFDGLSKQLETPPS--YTVGAYTT--VPPILGEQCLTPDGAPGMRWRVFNEPPGTPNRQH
                                                                                                                                                                                                                                                                                                                                                PGPWRDRGEKLVAAVREGKVKAETVRASARRILLLLERV----GAFEKAPDLAEHALDLPE
                                                                                                                                                                                                                                                                                                                                                                                                                     PGPPRFRGETLKFNVSNGKPFIHVIDQRAREVLQFVKKCAASGVTENGPEITVN--NTPE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVKAVMSSYNKLNGTYTSENPWLLTKVLREEWGFDGVVMSDWFGSHSTAETINAGLDLEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPGAFMTAYNGINGVSCSENPKYLDGMLRKEWGWDGLIMSDWYGTYSTTEAVVAGLDLEM 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGLGAAALIRGIQSTGVQATIKHFLCNDQEDRRMMVQSIVTERALREIYALPFQIAVRDS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCGTSLGSTFNQTLLEEAGKMMGKEATAKSAHVILGPTINMQRSPLGGRGFESIGEDPFL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDDILDKMTLEEQVSLLSGADFWTTVAIERLGVPKIKVTDGPNGARGGGSLVGGVKSACF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAACAVAYINGVQSQGVAATIKHFVANESEIERQTMSSDVDERTLREIYLPPFEEAVKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVATALGATWDPELIERAGVALGGQAKSKGASVLLAPTVNIHRSGLNGRNFECYSEDPAL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.9%; Score 1445.5; 40.5%; Pred. No. 8.86
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01-JAN-1990
01-JAN-1990
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=ATCC 27405 / DSM 1237;
MEDLINE=89364694; PubMed=2505054;
Graebhitz F., Ruecknagel K.P., Seiss M., Staudenbauer W.L.;
"Nucleotide sequence of the Clostridium thermocellum bgIB ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Thermostable beta-glucosidase B (EC 3.2.1.21)
(Cellobiase) (Beta-D-glucoside glucohydrolase)
                                                              PIR; S04381; S04381.
InterPro; IPR0012772; GH_3C.
InterPro; IPR001764; GH_3N.
Pfam; PF00933; Glyco_hydro_3; 1.
Pfam; PF01915; Glyco_hydro_3_C; 1.
PRINTS; PR00133; GLHYDRLASE3.
PROSITE; PS00775; GLYCOSYL_HYDROL_F3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol.
Hydrolase; Glycosidase; Cellulose degradation. ACT_SITE 231 231 BY SIMILARITY.
                                                                                                                                                                                                                                                                                      EMBL; X15644; CAA33665.1; -.
                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-glucosidases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding thermostable beta-glucosidase B: homology to beta-glucosidases.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YFPEDPYLSSELAASHIKGVQSQGVGACLKHFAANNQEHRRMTVDTIVDERTLKEIYFAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDIKKIIKQMTLEEKAGLCSGLDFWHTKPVERLGIPSIMMTDGPHGLRKQREDAEIADIN
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                                                                                                                                                      LRGKFTV 824
                                                                                                                                                                                                                 LQPGETKAVTIEEQEKYVAAYFDEERDQWCVEKGDY----EVIVSDSSAAKDGVA
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                                                                                                                                                                                    LNPGEEKTVTF-TLDKRAFAYYNTQIKDWHVESGEFLILIGRSSRDIVLKESYRVNSTVK
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Machida M., Ohtsuki I., Fukui S., Yamashita I.;
"Nucleotide sequences of Saccharomycopsis fibuligera
extracellular beta-glucosidases as expressed in Saccl
                                                                                                                                                                                                                                                              SEQUENCE
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PROSITE; PS00775; GLYCOSYL_HYDROL_F3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002772; GH_3C.
InterPro; IPR001764; GH_3N.
Pfam; PF00933; Glyco_hydro_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Last annotation update)
Beta-glucosidase 2 precursor (EC 3.2.1.21) (Gentiobiase) (Cellobiase)
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                        159 MVQSIVTERALREIYALPFQIAVRDSQPGAFMTAYNGINGVSCSENPKYLDGMLRKEWGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducin glucose residues with release of beta-D-glucose. PATHWAY: Cellulose degradation.
SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES.
SISANIPDRAMHELYLWPFADSIR-AGVGSVMCSYNRVNNTYSCENSYMINHLLKEELGF
                                                                                                                                                                     EAILKKLTLAEKVDLLAGIDFW-----HTKALPKHGVPSLRFTDGPNGVRGTKFFNGV 59
                                                                                                    ----YPSGMATGATFNKDLFLQRGQALGHEFNSKGVHIALGPAV----GPLGVKARGGRN 173
                                                                                                                                                     KALVSQMTIVEKVNLTTGTG-WQLGPCVGNTGSVPRFGIPNLCLQDGPLGVRLTDFSTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B45956; B45956.
                                                FEAFGSDPYLQGIAAAATIKGLQENNVMACVKHFIGNEQDIYRQPSNSKVDPEYDPATKE
                                                                          FESIGEDPFLAGLGAAALIRGIQSTGVQATIKHFLCNDQEDRRM-----
                                                                                                                            PAACFPCGTSLGSTFNQTLLEEAGKMMGKEAIAKSAHVILGPTINMQRSPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pF01915; Glyco_hydro_3_C; 1.
s; pR00133; GLHYDRLASE3.
                                                                                                                                                                                                            243;
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                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                   299
24
77
271
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336
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712
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24.5%;
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                                                                                                                                                                                                                                                            MW.
                                                                                                                                                                                                         118;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  degradation; Glycoprotein; Signal.
                                                                                                                                                                                                                    722; DB 1;
No. 5.6e-39;
                                                                                                                                                                                                                                                                                                                      (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                    (GLCNAC.
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                                                                                                                                                                                                                                                                                                            (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC.
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                                                                                                                                                                                                         267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
                                                                                                                                                                                                                                Length 880;
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292
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RESULT
BGL1_SA
ID BG
AC P2
DT 011
DT 011
DT 01
DT 05
DE 66
DE 66
DE 66
CS B6
OC E0
CC S0
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                            SEQUENCE FROM N.A.
MEDLINE-89133518; PubMed-3146949;
Machida M., Ohtsuki I., Fukui S.,
                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Beta-glucosidase 1 precursor (EC 3.2.1.21) (Gentiobiase) (Cellobiase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _SACFI
                                                                                                                                        Saccharomycetales;
NCBI_TaxID=4944;
                                                                                                                                                                                           Saccharomycopsis fibuligera (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BGL1_SACFI
        "Nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucose residues with release of beta-D-glucose.
PATHWAY: Cellulose degradation.
SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES
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                ALLRKYGNEGIVLLKNENNVLPLS -- KKKKTLI ---- VGPN--
                                                 ATRILAALYATNSFPTEDHLPNFSSWTTKEYGNKYYADNTTEIVKVNYNVDPSNDFTEDT
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STRAIN-LIZ / SSC1412 / ATCC 700720;
STRAIN-LIZ / SSC31412 / PubMed-11677609;
McClelland M., Sanderson K.E., Spieth J.,
Courtney L., Porwollik S., Ali J., Dante M.
Leonard S., Nguyen C., Scott K., Holmes A.
Ryan E., Sun H., Florea L., Miller W., Sto
                        Ryan E., Sun H., Florea L. Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                 Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Cellobiase) (Beta-D-glucoside BGLX OR STM2166.
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15-JUN-2002 (Rel. 41, Last annotation update)
Periplasmic beta-glucosidase precursor (EC 3.2.)
(Cellobiase) (Beta-D-glucoside glucohydrolase)
                                                                                                                                                                                                                SEQUENCE FROM N.A.
*Complete genome sequence of Salmonella
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                                                    Dante M., Du F., Hou S., I olmes A., Grewal N., Mulvan W., Stoneking T., Nhan M.,
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     enterica serovar Typhimurium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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InterPro; IPR002772; GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 413:852-856(2001).
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
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                               424 KTDMHLVDYYHPKAADTWYADMEGTYTADEDCTYELGLVVCGTAKAYVDDQLVVDNATKQ 483
                                                                                              364 GLSKQLETPPSYTVGAYTTVPPILGEQCLTPDGAPGMRWRVFNEPPGTPNRQHIDELFFT
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                                                                                                                           KEAREVARESVVLLKNRLETLPLKKSGTIAVVGPLADSQRDVMGSWSAA---
                                                                                                                                                            ALLRKVGNEGIVLLKNENNVLPLSKKKKTLIVGPNA-KQATYHGGGSAALRAYYAVTPFD
                                                                                                                                                                                            SKYLPGLIKSGKVTMAELDDATRHVLNVKYDMGLFNDPYSHLGPKESDPVDTNAESRLHR
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PF01915; Glyco_hydro_3_C; 1.
PF01915; GLYCOSYL_HYDROL_F3;
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BY SIMILARITY.
R -> L (IN REF. 1).
EA -> KP (IN REF. 1).
V -> F (IN REF. 1).
E -> K (IN REF. 1).
E -> K (IN REF. 1).
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BGLX_ECOLI
ID BGLX_E
AC P3363
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DE CCELLO
CC STRAIN
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BGLX_ECOLI

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P33363;

T 01-FEB-1994 (Rel. 28, Created)

T 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Periplasmic beta-glucosidase precursor (EC 3.2.1.21)

"~allobiase) (Beta-D-glucoside glucohydrolase).

"Alvision; Enterv
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                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
-i- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reduc
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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STRAIN=K12 / MG1655;
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STRAIN=K12 / BHB2600;
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Submitted (SEP-1994)
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Yang M., Luoh S., G
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                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing glucose residues with release of beta-D-glucose. SUBCELLULAR LOCATION: Periplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPIDIE----ALKEWNQQMKYDAEPGKENVFIGVDSARVKQG
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EMBL; U00007; AAA60495.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00933; Glyco_hydro_3; 1.
Pfam; PF01915; Glyco_hydro_3_C; 1.
PRINTS; PR00133; GLHYDRLASE3.
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Hydrolase; Glycosidase; Periplasmic; Signal; Complete proteome.
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InterPro; IPR001764; GH_3N.
                                                                                                                                                                        489
                                                                                                                                                                                                          542
                                                                                                                                                                                                                                                                                                                                                                                                               365 LSKQLETPPSYTVGAYTTVPPILGEQCLTPDGAPGMRWRVFNEPPGTPNRQHIDELFFTK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 ALLRKYGNEGIVLLKNENNVLPLSKKKKTLIYGPNAKQATYHGGGSAALRAYYAVTPFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 SKYLPGLIKSGKVTMAELDDAARHVLNVKYDMGLFNDPYSHLGPKESDPVDTNAESRLHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 KHFAAYGAVEGGKEYNTVDMSPQRLFNDYMPPYKAGL-DAGSGAVMVALNSLNGTPATSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 DDGLNMTWAPMVDVSRDPRWGRASEGFGEDTYLTSTMGKTMVEAMQGKSPADRYSVMTSV
                                     605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 PKYLDGMLRKEWGWDGLIMSDW------YGTYSTTE-----AVVAGLDLEMPGPPRFR 251
                                                       661 DNPAFLNFRTBAGRTLYGEDVYVGY--RYYEFADKDVNFPFGHGLSYTTFAFSNLSVS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 DIRAMQDQVMELSRLKIPLFFAYDVLHGQRTVFPISLGLASSFNLDAVKTVGRVSAYEAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIDVEAILKKLTLAEKVDLLAGIDFWHTKALPKHGVPSLRFTDGPNGVRGTKFFNGV--- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAFVTELLKKMTVDEKIGQLRLISVGPDN--PKEAIREM-IKDGQVGA----IFNTVTRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWLLKDVLRDQWGFKGITVSDHGAIKELIKHGTAADPEDAVRVALKSGINMSM--SDEYY
                                   QIPVYYS-HLNTGRP-YNADKPNKYTSRYFDEANGAL-YPFGYGLSYTTFTVSDVKLSAP
                                                                                                                                        TVVVMQTGTPEEMPWLD-ATPAVIQAWYGGNETGNSIADVVFGDYNPSGKLSLSFPKRLQ
                                                                                                                                                                                                        VIDDQAEIEKSVALAKEHDQVIICAGLNADWETEGADRASMKLPGVLDQLIADVAAANPN
                                                                                                                                                                                                                                                                                                                                             TDMHLVDYYHPKAADTWYADMEGTYTADEDCTYELGLVVCGTAKAYVDDQLVVDNATKQV 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEAREVARESLYLLKNRLETLPLKKSATIAVVGPLAD---
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                                                                                                    ----QEMIDEAVQTAKQSDVVVAVVGEAQGMAHEASSRTDITIPQSQRDLIAALKATGKP
                                                                                                                                                                                                                                            VG-----ENGKVLYAKGANVTSDKGIIDFLNQYEEAVKVDPRSP
                                                                                                                                                                                                                                                                           PGDAFFGSATREETGRINLVKG----NTYKFKIEFGSAPTYTLKGDTIVPGHGSLRVGGCK 541
--HKDGKLSVSLSVKNTGSVPGAQVAQLYVKPLQAAKINRPVKELKGFAKVELQPGETKA 774
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287
765 AA;
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287 I
83460 MW;
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24.9%;
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Pred. No. 1.8e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERIPLASMIC BETA-GLUCOSIDASE.
BY SIMILARITY.
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RESULT 8
BGLS_HANAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nucleotide sequence of Candida pelliculosa beta-glucosidase gene.";
Nucleic Acids Res. 13:6273-6282(1985).

-i- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-glucose residues with release of beta-D-glucose.

-i- PARHWAY: Cellulose degradation.

-i- SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Beta D-glucoside glucohydrolase).
Hansenula anomala (Yeast) (Candida pelliculosa).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Beta-glucosidase precursor (EC 3.2.1.21) (Gentiobiase) (Cellobiase)
                                                                                                                           CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BGLS_HANAN
                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-86016087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P06835;
                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kohchi C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Acetaetherius;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                CARBOHYD
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SIGNAL
                                                                                                                                                                                                                                                                                            pfam; pf00933; Glyco_hydro_3; 1.
pfam; pf01915; Glyco_hydro_3_C; 1.
primts; pf010133; GLHYDRLASE3.
prosite; pf00775; GLYCOSYL_HYDROL_F3; 1.
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X02903; CAA26662.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toh-E A.;
                                                                                                                                                                                                                                                                                 Glycosidase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=2995925;
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                                                                                                                                                                                                                                                                                 Cellulose degradation; Glycoprotein; Signal
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01-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILKKLTLAEKVDLLAGID-----FWHTKALPKHGVPSLRFTDGPNGVRGTKFFNGVPAA 62
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 (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 41, Last annotation updat
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                                                  STANDARD;
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                                                PRT;
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pfam; PF00933; Glyco_hydro_3; 1.
pfam; PF01915; Glyco_hydro_3_C; 1.
prinvs; PR00133; GLHYDRUSE3:
PROSITE; PS00775; GLYCOSYL_HYDROL_F3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Glycosidase; Cellulose degradation; Glycoprotein; Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergilus aculeatus.*;

Gene 173:287-288(1996).
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing glucose residues with release of beta-D-glucose.
-!- PATHWAY: Cellulose degradation.
-!- SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES.
167 RALREIYALPFQIAVRDSQPGAFMTAYNGINGVSCSENPKYLDGMLRKEWGWDGLIMSDW
                                                                                                                                103 NSAFPAGVNVAATWDKNLAYLRGQAMGQEFSDKGIDVQLGPAAGPLGRSPDGGRNWEGFS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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Ooi T., Arai M.
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                                                                                                                                                                             61 AACFPCGTSLGSTFNQTLLEEAGKMMGKEAIAKSAHVILGPTIN-MQRSPLGGRGFESIG 119
                                                                                                                                                                                                                       49 AIVSQMTLDEKVNLTTGTG-WELEKCVGQTGGVPRLNIGGMCLQDSPLGIRDSDY----- 102
                                                                                                                                                                                                                                                                 8 AILKKLTLAEKVDLLAGIDFW-----HTKALPKHGVPSLRFTDGPNGVRGTKFFNGVP 60
                                                                                         EDPFLAGLGAAALIRGIQSTGVQATIKHFLCNDQEDRRMM-------VQSIVTE 166
                                            PDPALTGVLFAETIKGIQDAGVVATAKHYILNEQEHFRQVAEAAGYGFNISDTISSNVDD
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                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           860 AA;
                                                                                                                                                                                                                                                                                                                  Conservative 114;
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93052 MW;
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Pred. No. 7e-30;
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BGLS_BUTFI
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01-APR-1990 (Rel. 14, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
Beta-glucosidase A (EC 3.2.1.21) (Gentiobiase)
                                                                                                                                                                                                                                                               BUTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 LLKN-NNALPLTGKERKVAILGEDAGSNSY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 LIKNENNVLPLS-KKKKTLIVGPNAKQATYHGGGSAALRAYYAVTPFDGLSKQLETPPSY 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 YKYGRDRLYQPPNFSSWTRDEYGFKYFYPQEGPYEKVNHFVNVQRNHSEVIRKLGADSTV 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 KKCAASGV-----AALLRKVGNEGIV 316
                                                                                Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;
                                                                                                                                    glucoside glucohydrolase).
                                                                                                                                                                                                                                         BGLS_BUTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 KAADTWYADMEGTYTADEDCTYELGLVVCGTAKAYVDDQLVVDNATKQVPGDAFFGSATR 495
STRAIN-H17C
                    SEQUENCE FROM N.A.
                                                                    Butyrivibrio
                                                                                                   Butyrivibrio fibrisolvens
                                                                                                                       BGLA.
                                                                                                                                                                                                                            P16084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 IHSVGPVLVDEWYDHPNVTAILWAGLPGQESGNSLADVLYGRVNPGAKSPFTWGKTREAY 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        668 NASSNAQVATETGAAPTFGQVGNASDYVYPEGLTRISKFTYPWLNSTDLKASSGDPYYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          608 GDYLVRELNNGNGAPODDFSEGVFIDYRGFDKRNETPIYEFGHGLSYTTFNYSGLHIQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               663 PAF----LNFRTEAGRTLYGEDVYVGYRYYEFADKDVNFPFGHGLSYTTFAFSNLSV---
                                                 NCBI_TaxID=831;
                                                                                                                                                                                                                                                                                                                                 844 GSSS 847
                                                                                                                                                                                                                                                                                                                                                                                                                                   747 LQAAKINRPVKELKGFAKVELQPGETKAVTIEEQEKYVAAYFDEERDQWCVEKGDYEVIV 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    728 DTAEHVPEGATDGSPQPVLPAGGGSGGNPRLYDELIRVSVTVKNTGRVAGDAVPQLYV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAHHSGVGSALAGLDMSMPGDITFDSATSFWGTNLTIAVLNGTVPQWRVDDMAVRIMAAY 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YGTYSTTEAVVAGLDLEMPG-----PPRFRGETLKFNVSNGKPFIHVIDQRAREVLQFV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVGAYTTVPPILGEQCLTPDGAPGMRWRVFNEPPGTPNRQHIDELFFTKTDMHLVDYYHP 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOTGTPEEM-PWLDATPAVIOAWYG--GNETGNSIADVVFGDYNPSGKLSLSFPKRLQDN 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKQASVSLVFVNSDAG----EGYISVDGNEGDRNNLTLWKNGDNLIK--AAANNCNNTIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EETGRINLVKGNTYKFKIEFGSAPTYTLKGDTIVPGHGSLRVGGCKVIDDQAEIEKSVAL 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKEHDQVIICAGLNADWETEG-----ADRASMKLPGVLDQLIADVAAAN--PNTVVV 605
                                                                                                                                                                                                                                                                                                                                                                                                 -SLGGPNEPKVVLRKFDRLTLKPSEETVWTTTLTRRDLSNW-DVAAQDWVITSYPKKVHV 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SHKDGK------746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FPYLVTPEQAIQAEVL-----KHKGSVYAITDNWALSQVETL 492
                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                830 AA.
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                                                                                                                                                            (Cellobiase) (Beta-D-
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91086918; PubMed-2262790;
Lin L.L., Rumbak E., Zappe H., Thompson J.A., Woods D.R.;
Cloning, sequencing and analysis of expression of a Butyrivibrio fibrisolvens gene encoding a beta-glucosidase.";
J. Gen. Microbiol. 136:1567-1576(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content; is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-glucose residues with release of beta-D-glucose.
-i- SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: B.FIBRISOLVENS BETA-GLUCOSIDASE HYDROLYSES CELLOBIOSE
TO A LIMITED EXTENT, CELLOTRIOSE TO CELLOBIOSE AND GLUCOSE, AND
CELLOTETRAOSE AND CELLOPENTAOSE TO PREDOMINANTLY GLUCOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00933; Glyco_hydro_3; 1.
Pfam; PF01915; Glyco_hydro_3_C; 1.
PRINTS; PR00133; GLHYDRLLASE3.
PROSITE; PS00775; GLYCOSYL_HYDROL_F3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                 _RUMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Glycosidase; Cellulose degradation.
ACT_SITE 769 769 BY SIMILARITY.
                                                                                                                                               P15885;
01-ApR-1990 (Rel. 14, Created)
01-ApR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Beta-glucosidase (EC 3.2.1.21) (Gentiobiase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002772; GH_3C.
InterPro; IPR001764; GH_3N.
                                                                                     Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543 VTLEDFIAQLSNEQLASLLGGQPNVGMANTFGYGNLPEVGVPNAQTCDGPAGVRIAPEV- 601
                   SEQUENCE FROM N.A.
                                                                                                             Ruminococcus albus
                                                                                                                               glucoside glucohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 GVVTTAFPCSTLLACTWNEDICYEVGVAGGEEAKECNFGAWLTPAVNIHRSPLCGRNFEY 661
   STRAIN-F-40;
                                                     NCBI_TaxID=1264;
                                                                           Ruminococcus
                                                                                                                                                                                                                                                                                                                                                                                                              722 EIIVKEQSPGASCLQYNIVNGQRSSESHDLLTGILRDEWGFEGVVVSDWWGFGEHYKEVL 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662 YSEDPFLAGKQAAAMVRGIQSNNIIATPKHFALNNKESNRKGSDSRASERAIREIYLKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 IGEDPFLAGLGAAALIRGIQSTGVQATIKHFLCNDQEDRRMMVQSIVTERALREIYALPF 177
                                                                                                                                                                                                                                                                                                                                      782 AGNDIKM 788
                                                                                                                                                                                                                                                                                                                                                                            238 AGLDLEM 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIAVRDSQPGAFMTAYNGINGVSCSENPKYLDGMLRKEWGWDGLIMSDWYGTYSTTEAVV 237
                                                                                                                                                                                                                                               RUMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               830 AA;
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                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; Score 451.5; DB 1;
41.3%; Pred. No. 1.5e-21;
41.3%; Pred. No. 1.5e-21;
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                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                     947 AA
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                                                                                                                                                         (Cellobiase) (Beta-D-
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                                                                                                                                              01-FEB-1995
01-FEB-1995
15-JUN-2002
                 SEQUENCE FROM N.A
                                                                 Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
STRAIN=BD99 / MS94;
                                                                                                                       Hypothetical lipoprotein ybbD precursor (ORF1).
                                                                                                                                                                                                       P40406;
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Pfam; PF01915; Glyco_hydro_3_C; 1.
PRINTS; PR00133; GLYCONTL_HYDROL_F3; 1.
PROSITE; PS00775; GLYCOSYL_HYDROL_F3; 1.
Hydrolase; Glycosidase; Cellulose degradation.
ACT_SITE 696 696 BY SIMILARITY.
                                                                                                                                                                                                                         YBBD_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "DNA sequence of a beta-glucosidase from Ruminococcus albus.",
Nucleic Acids Res. 18:671-671(1990).
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-p-
glucose residues with release of beta-D-glucose.
-!- PATHWAY: Cellulose degradation.
                                                                                                                                                                                                                                                                                                               776 EAVEVINK 783
                                                                                                                                                                                                                                                                                                                                                  314 GIVLLKNE 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                559 LEMRANKVDCLLGPGMNIHRHPLNGRNFEYFSEDPFLTGTMAAAELEGLHSVGVEGTIKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90175009; PubMed=2106673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 KALPKHGVPSLRFTDGPNGVR----GTKFFNGVPAACFPCGTSLGSTFNQTLLEEAGKMMG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                               NVIAALADGRLTRAELQRSARNILSFMM-------STHAMARKLGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDGMLRKEWGWDGLIMSDWYGTYST-----TEAVVAGLDLEMPGPPRFRGETLKF 257
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                                                                                                                                                                                                                                                                                                                                                                                                                 NV----SNGKPFIHVIDQRAREVLQFVKKCAASGVTENGPETTVNNTPETAALLRKVGNE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLCNDQEDRRMMYQSIVTERALREIYALPFQIAVRDSQPGAFMTAYNGINGVSCSENPKY 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEAIAKSAHVILGPTINMQRSPLGGRGFESIGEDPFLAGLGAAALIRGIQSTGVQATIKH 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHLEELGIPAGCCSDGPSGMRLDVGTKAFS-----LPNGTLIAATFNKSLITELFTYLG
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                                                                                                                                      (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     947 AA; 104277 MW; C43B8CDD9D60A115 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takano M., Shimizu S.;
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                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.7%; Score 425; DB 1; 34.7%; Pred. No. 9.6e-20;
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                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                     642 AA
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RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Iiu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche R., Scoffone F.,
RA Sato T., Scanlan E., Schletch S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schletch S., Schroeter R., Scoffone F.,
RA Sakiguchi J., Sekowska A., Seror S.J., Serror P., Shin P.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Viaria A., Wambutt R., Wedler E., Scomane K., Yasumoto K., Yata K.,
RY The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                     EMBL; L19954; AAA64351.1; -.
                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:249-256(1997).
-i- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES
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Subtilist; BG10832; ybbD.
InterPro; IPR002772; GH\_3C.
InterPro; IPR001764; GH\_3N.
InterPro; IPR001764; GH\_3N.
InterPro; IPR001764; GH\_3N.
InterPro; IPR001764; GH\_3N.
InterPro; IPR001765; Glyco\_hydro\_3 C; 1.
InterPro; IPR001765; GLYCOSYL\_HYDROL\_F3; 1.
IPROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.
INTERPROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.

z99104;

AB002150; BAA19499.1; -. CAB11942.1; -.

Hypothetical protein; Hydrolase; Glycosidase; Membrane; Lipoprotein;

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ACT_SITE
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                                                                                                                                                                                                                                                               (Beta-D-glucoside glucohydrolase) (Fragment). Schizophyllum commune (Bracket fungus). Eukaryota; Fungi; Basidiomycota; Hymenomycete
                                                                                                                                                                                                                                                                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Beta-glucosidase (EC 3.2.1.21) (Gentiobiase)
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                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=86295810; PubMed=3091028;
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                                                            n a yeast beta-glucosidase.";
chem. Int. 12:905-912(1986).
CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing
glucose residues with release of beta-D-glucose.
PATHWAY: Cellulose degradation.
SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES.
             European Bioinformatics Institute.
                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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N-ACYL DIGLYCERIDE (POTENTIAL)
BY SIMILARITY.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=E1 Tor N16961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Beta-hexosaminidase (EC 3.2.1.52) (N-acety1-beta-glucosaminidase)
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16-OCT-2001
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InterPro; IPR001764; GH_3N.
pfam; pF01915; Gly9co_hydro_3_C; 1.
pROSITE; PS00775; GLYCOSYL_HYDROL_F3; PARTIAL.
Hydrolase; Glycosidase; Cellulose degradation;
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                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restricted the companies of the control of the companies of the control of the
                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).
-i- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-acetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "DNA sequence of both cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser C.M.;
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                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO FAMILY 3
                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES. NAGZ
                                                                                                                                                                                                                                                                  SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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Pred. No. 0.
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                                                                                                                                                                                       a collaboration
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb+sib.ch/announce/or send an email to license@isb-sib.ch).

There are no restrictions

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EMBL; AE004155; AAF93857.1;

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                            Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

-i-FUNCTION: Cleaves GlcNAc linked beta-1.4 to MurNAc tripeptides (By similarity). HYDROLYZES RAPIDLY P-NITROPHENYL-N-ACETYL-BETA-D-GLUCOSAMINIDE (PNP-BETA-GLCNAC) AND 4-METHYLUMBELLLTERYL-BETA-GLCNAC, AND SLIGHTLY ACTIVE ON P-NITROPHENYL-BETA-GALNAC. MAY PLAY A ROLE IN SIGNAL TRANSDUCTION BETWEEN HOST AND ORGANISM.
-i- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-acetyl-b-hexosamine residues in N-acetyl-beta-b-hexosaminides.
-i- ENZYME REGULATION: INHIBITED BY GLCNAC, 2-ACETAMIDO-1-N-(4-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Beta-hexosaminidase (EC 3.2.1.52) (N-acetyl-beta-glucosaminidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pfam; PF00933; Glyco_hydro_3; 1.

PROSITE; PS00775; GLYCOSYL_HYDROL_F3; 1.

Hydrolase; Glycosidase; Peptidoglycan synthesis; Cell division; Cell wall; Complete proteome.

ACT_SITE 242 242 BY SIMILARITY.
                                                                                                                                                                                                                               "Molecular cloning and characterization of a glucosaminidase from Vibrio furnissii."; J. Biol. Chem. 271:33433-33439(1996).
                                                                                                                                                                                Chitlaru E.,
                                                                                                                                                                                                                                                                            Chitlaru E.,
                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                          Vibrio furnissii
                                                                                                                                                                                                 REVISIONS TO 70-80.
                                                                                                                                                                                                                                                                                               MEDLINE=97125984; PubMed=8969206;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=29494;
                                                                                                                                                                                                                                                                                                                                                                                                              NAGZ OR EXO II
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ASPARTYL)-2-DEOXY-BETA-D-GLUCOPYRANOSYLAMINE (GLCNAC-ASN) AND (2-ACETAMIDO-2-DEOXY-D-GLUCOPYRANOSYLIDENE)-AMINO-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KREAAVEVLDNLP---IMEVPQAEALLKK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLGAAALIRGIQSTGVQATIKHF-------LCNDQEDRRMMVQSIVTERALREIYA 174
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, A737BD82C149D3A2 CRC64;
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Best Local
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Pfam; PF00933; Glyco_hydro_3; 1.
PROSITE; PS00775; GLYCOSYL_HYDROL_F3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
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ARE 7.0 AND 45 DEGREES CELSIUS.
-I- SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES. NAGZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: CELL WALL SYNTHESIS; MUREIN TRIPEPTIDE RECYCLING PATHWAY.
-!- SUBUNIT: MONOMER (POTENTIAL).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- MISCELLANEOUS: MAXIMAL PH AND OPTIMAL TEMPERATURE OF THE ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U52818; AAC44686.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHENYLCARBAMATE (PUGNAC)
V---PQAQSLLKQ
                                VNNTPETAALLRK
                                                                                                                                                                                                                         RGIQSTGVQATIKHF------LCNDQEDRRMMVQSIVTERALREIYALPFQIAVR 182
                                                                                                                                                                                                                                                                                       QTLLEEAGKMMGKEAIAKSAHVILGPTIN--MQRSPLGGRGFESIGEDPFLAGLGAAALI 133
                                                                                                                                                                                                                                                                                                                         AAKRPILIGVD-----QEGGRVQRFRDG-----FSKIPAAQLYARSDNGT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                              ----DLSMEGAAIMGGPAERAQQS------LDAGCDMVLMCNKRESAVAVLDQLPISV
                                                                                            VAGLDLEMPGPPRFRGETLKFNVSNGKPFIHVIDQRAREVLQFVKKCAASGVTENGPETT
                                                                                                                                                                                           RGMKSVGMATTGKHFPGHGAVIADSHLETPYDERDSIADDMTIFRAQIEAGILDNMMPAH
                                                                                                                                                                                                                                                         -QLAEDGGWLMAAELIAHDIDLSFAPVLDKGFDCRAIGNRAF---GDDVQTVLTYSSAYM
                                                                                                                                                           ---- DSQPGAFMTAYNGINGVSCSENPKYLDGMLRKEWGWDGLIMSDWYGTYSTTEAV
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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329 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        242
36181 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                        3.4%;
                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                            -ASGSPYWLKQVLRQELGFQGIVFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 147.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      440C6A9B18143C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        0.018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                        114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        329;
                                                                                                                                                                                                                                                                                                                                                                                        83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     commercial
                                                                                                                                                            236
                                                                290
                                                                                                296
                                                                                                                                                                                                                                                           147
                                                                                                                            242
                                                                                                                                                                                                                                                                                                                           91
                                                                                                                                                                                                                                                                                                                                                                                        11;
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earch completed: April 26, 2003, 13:08:55 ob time : 36 secs